

## SEQUENCE LISTING

<110> Cargill Incorporated

<120> PRODUCTION OF 3-HYDROXYPROPIONIC ACID USING BETA  
-ALANINE/PYRUVATE AMINOTRANSFERASE

<130> 66576-02

<160> 28

<170> PatentIn version 3.2

<210> 1

<211> 60

<212> DNA

<213> Artificial

<220>

<223> PCR primer

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27

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atcg 64

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<210> 17

<211> 1347

<212> DNA

<213> Pseudomonas putida

<220>

<221> CDS

<222> (1)..(1344)

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ctg gac gcc cac tgg atg ccc tac acc gcc aac cgc aac ttc cag cgc 96  
Leu Asp Ala His Trp Met Pro Tyr Thr Ala Asn Arg Asn Phe Gln Arg  
20 25 30

gac cca cgc ctg atc gtg gcg gcc gaa ggc aac tac ctg gtc gat gac 144  
Asp Pro Arg Leu Ile Val Ala Ala Glu Gly Asn Tyr Leu Val Asp Asp  
35 40 45

cac ggg cgc aag atc ttc gac gcc ctg tcc ggc ctg tgg acc tgc ggc 192  
His Gly Arg Lys Ile Phe Asp Ala Leu Ser Gly Leu Trp Thr Cys Gly  
50 55 60

gca ggg cac act cgc aag gaa atc gct gac gcg gtg acc cgt caa ctg 240  
Ala Gly His Thr Arg Lys Glu Ile Ala Asp Ala Val Thr Arg Gln Leu

65	70				75				80				
agt acg ctg gac tac tcc cca gcg ttc cag ttc ggc cac ccg ctg tcg	Ser Thr Leu Asp Tyr Ser Pro Ala Phe Gln Phe Gly His Pro Leu Ser				85				90				288
ttc cag ctg gcg gaa aag atc gcc gag ctg gtt ccg ggc aat ctg aat	Phe Gln Leu Ala Glu Lys Ile Ala Glu Leu Val Pro Gly Asn Leu Asn				100				105				336
cac gtc ttc tat acc aac tcc ggt tcc gag tgc gcc gat acc gca ctg	His Val Phe Tyr Thr Asn Ser Gly Ser Glu Cys Ala Asp Thr Ala Leu				115				120				384
aag atg gtg cgt gcc tac tgg cgc ctg aaa ggc cag gca acc aag acc	Lys Met Val Arg Ala Tyr Trp Arg Leu Lys Gly Gln Ala Thr Lys Thr				130				135				432
aag atc atc ggc cgt gcc cgt ggt tac cat ggc gtg aac atc gcc ggt	Lys Ile Ile Gly Arg Ala Arg Gly Tyr His Gly Val Asn Ile Ala Gly				145				150				480
acc agc ctg ggt ggc gtc aac ggt aac cgc aag atg ttt ggc cag ctg	Thr Ser Leu Gly Gly Val Asn Gly Asn Arg Lys Met Phe Gly Gln Leu				165				170				528
ctg gac gtc gac cac ctg cct cac act gta ttg ccg gtg aac gcc ttc	Leu Asp Val Asp His Leu Pro His Thr Val Leu Pro Val Asn Ala Phe				180				185				576
tcg aaa ggc ttg ccg gaa gag ggc ggt atc gcg ctg gct gac gaa atg	Ser Lys Gly Leu Pro Glu Glu Gly Gly Ile Ala Leu Ala Asp Glu Met				195				200				624
ctc aag ctg atc gag ctg cac gat gcc tcc aac atc gca gca gtc atc	Leu Lys Leu Ile Glu Leu His Asp Ala Ser Asn Ile Ala Ala Val Ile				210				215				672
gtc gag ccg ctg gcc ggt tcg gcc ggt gtg ctg ccg ccg cca aag ggt	Val Glu Pro Leu Ala Gly Ser Ala Gly Val Leu Pro Pro Pro Lys Gly				225				230				720
tac ctg aag cgc ctg cgt gaa atc tgc acc cag cac aac att ctg ctg	Tyr Leu Lys Arg Leu Arg Glu Ile Cys Thr Gln His Asn Ile Leu Leu				245				250				768
atc ttc gac gaa gtg atc aca ggc ttc ggc cgc atg ggc gcg atg acc	Ile Phe Asp Glu Val Ile Thr Gly Phe Gly Arg Met Gly Ala Met Thr				260				265				816
ggc tcg gaa gcc ttc ggc gtt acc ccg gac ctg atg tgc atc gcc aag	Gly Ser Glu Ala Phe Gly Val Thr Pro Asp Leu Met Cys Ile Ala Lys				275				280				864
cag gtg acc aac ggc gcc atc ccg atg ggc gca gtg att gcc agc agc	Gln Val Thr Asn Gly Ala Ile Pro Met Gly Ala Val Ile Ala Ser Ser				290				295				912
gag atc tac cag acc ttc atg aac cag ccg acc ccg gaa tac gcc gtg	Glu Ile Tyr Gln Thr Phe Met Asn Gln Pro Thr Pro Glu Tyr Ala Val				305				310				960
													315
													320

gaa ttc cca cac ggc tac acc tat tcg gcg cac ccg gta gcc tgt gcc 1008  
 Glu Phe Pro His Gly Tyr Thr Tyr Ser Ala His Pro Val Ala Cys Ala  
 325 330 335

gcc ggt ctc gcc gcg ctg gac ctg ctg cag aag gaa aac ctg gtg cag 1056  
 Ala Gly Leu Ala Ala Leu Asp Leu Leu Gln Lys Glu Asn Leu Val Gln  
 340 345 350

tcc gcg gct gaa ctg gcg ccg cat ttc gag aag ctg ctg cac ggc gtg 1104  
 Ser Ala Ala Glu Leu Ala Pro His Phe Glu Lys Leu Leu His Gly Val  
 355 360 365

aag ggc acc aag aat atc gtc gat atc cgc aac tac ggc ctg gcc ggc 1152  
 Lys Gly Thr Lys Asn Ile Val Asp Ile Arg Asn Tyr Gly Leu Ala Gly  
 370 375 380

gcc atc cag atc gcc gcc cgt gac ggt gat gcc atc gtt cgc cct tac 1200  
 Ala Ile Gln Ile Ala Ala Arg Asp Gly Asp Ala Ile Val Arg Pro Tyr  
 385 390 395 400

gaa gcg gcc atg aag ctg tgg aaa gcg ggc ttc tat gta cgc ttt ggt 1248  
 Glu Ala Ala Met Lys Leu Trp Lys Ala Gly Phe Tyr Val Arg Phe Gly  
 405 410 415

ggc gac acc ctg cag ttc ggc cca acc ttc aat acc aag ccg cag gaa 1296  
 Gly Asp Thr Leu Gln Phe Gly Pro Thr Phe Asn Thr Lys Pro Gln Glu  
 420 425 430

ctg gac cgc ttg ttc gat gct gtt ggc gaa acc ctg aac ctg atc gac 1344  
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 435 440 445

tga 1347

<210> 18  
 <211> 448  
 <212> PRT  
 <213> *Pseudomonas putida*

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Leu Asp Ala His Trp Met Pro Tyr Thr Ala Asn Arg Asn Phe Gln Arg  
 20 25 30

Asp Pro Arg Leu Ile Val Ala Ala Glu Gly Asn Tyr Leu Val Asp Asp  
 35 40 45

His Gly Arg Lys Ile Phe Asp Ala Leu Ser Gly Leu Trp Thr Cys Gly  
 50 55 60

Ala Gly His Thr Arg Lys Glu Ile Ala Asp Ala Val Thr Arg Gln Leu  
 65 70 75 80

Ser Thr Leu Asp Tyr Ser Pro Ala Phe Gln Phe Gly His Pro Leu Ser  
 85 90 95

Phe Gln Leu Ala Glu Lys Ile Ala Glu Leu Val Pro Gly Asn Leu Asn  
 100 105 110

His Val Phe Tyr Thr Asn Ser Gly Ser Glu Cys Ala Asp Thr Ala Leu  
 115 120 125

Lys Met Val Arg Ala Tyr Trp Arg Leu Lys Gly Gln Ala Thr Lys Thr  
 130 135 140

Lys Ile Ile Gly Arg Ala Arg Gly Tyr His Gly Val Asn Ile Ala Gly  
 145 150 155 160

Thr Ser Leu Gly Gly Val Asn Gly Asn Arg Lys Met Phe Gly Gln Leu  
 165 170 175

Leu Asp Val Asp His Leu Pro His Thr Val Leu Pro Val Asn Ala Phe  
 180 185 190

Ser Lys Gly Leu Pro Glu Glu Gly Gly Ile Ala Leu Ala Asp Glu Met  
 195 200 205

Leu Lys Leu Ile Glu Leu His Asp Ala Ser Asn Ile Ala Ala Val Ile  
 210 215 220

Val Glu Pro Leu Ala Gly Ser Ala Gly Val Leu Pro Pro Pro Lys Gly  
 225 230 235 240

Tyr Leu Lys Arg Leu Arg Glu Ile Cys Thr Gln His Asn Ile Leu Leu  
 245 250 255

Ile Phe Asp Glu Val Ile Thr Gly Phe Gly Arg Met Gly Ala Met Thr  
 260 265 270

Gly Ser Glu Ala Phe Gly Val Thr Pro Asp Leu Met Cys Ile Ala Lys  
 275 280 285

Gln Val Thr Asn Gly Ala Ile Pro Met Gly Ala Val Ile Ala Ser Ser  
 290 295 300

Glu Ile Tyr Gln Thr Phe Met Asn Gln Pro Thr Pro Glu Tyr Ala Val  
 305 310 315 320

Glu Phe Pro His Gly Tyr Thr Tyr Ser Ala His Pro Val Ala Cys Ala  
 325 330 335

Ala Gly Leu Ala Ala Leu Asp Leu Leu Gln Lys Glu Asn Leu Val Gln  
 340 345 350

Ser Ala Ala Glu Leu Ala Pro His Phe Glu Lys Leu Leu His Gly Val  
 355 360 365

Lys Gly Thr Lys Asn Ile Val Asp Ile Arg Asn Tyr Gly Leu Ala Gly  
 370 375 380

Ala Ile Gln Ile Ala Ala Arg Asp Gly Asp Ala Ile Val Arg Pro Tyr  
 385 390 395 400

Glu Ala Ala Met Lys Leu Trp Lys Ala Gly Phe Tyr Val Arg Phe Gly  
 405 410 415

Gly Asp Thr Leu Gln Phe Gly Pro Thr Phe Asn Thr Lys Pro Gln Glu  
 420 425 430

Leu Asp Arg Leu Phe Asp Ala Val Gly Glu Thr Leu Asn Leu Ile Asp  
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<210> 19

<211> 1347

<212> DNA

<213> Pseudomonas aeruginosa

<220>

<221> CDS

<222> (1)..(1344)

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ctg cgc gcc cac tgg atg ccc ttc tcc gcc aac cgc aac ttc cag aag 96  
 Leu Arg Ala His Trp Met Pro Phe Ser Ala Asn Arg Asn Phe Gln Lys  
 20 25 30

gac ccg cgg atc atc gtc gcc gcc gaa ggc agc tgg ctg acc gac gac 144  
 Asp Pro Arg Ile Ile Val Ala Ala Glu Gly Ser Trp Leu Thr Asp Asp  
 35 40 45

aag ggc cgc aag gtc tac gac agc ctg tcc ggc ctg tgg acc tgc ggc 192  
 Lys Gly Arg Lys Val Tyr Asp Ser Leu Ser Gly Leu Trp Thr Cys Gly  
 50 55 60

gcc ggc cac tcg cgc aag gaa atc cag gag gcg gtg gct cgc cag ctc 240



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Ala 65	Gly	His	Ser	Arg	Lys 70	Glu	Ile	Gln	Glu	Ala 75	Val	Ala	Arg	Gln	Leu 80	
ggc	acc	ctc	gac	tac	tcg	ccg	ggc	ttc	cag	tac	ggc	cat	ccg	ctg	tcc	288
Gly	Thr	Leu	Asp	Tyr	Ser	Pro	Gly	Phe	Gln	Tyr	Gly	His	Pro	Leu	Ser	
				85					90					95		
ttc	cag	ttg	gcc	gag	aag	atc	gcc	ggg	ttg	ctg	cca	ggc	gaa	ctg	aac	336
Phe	Gln	Leu	Ala	Glu	Lys	Ile	Ala	Gly	Leu	Leu	Pro	Gly	Glu	Leu	Asn	
			100					105					110			
cac	gtg	ttc	ttc	acc	ggg	tcc	ggc	tcc	gag	tgc	gcc	gac	acc	tcg	atc	384
His	Val	Phe	Phe	Thr	Gly	Ser	Gly	Ser	Glu	Cys	Ala	Asp	Thr	Ser	Ile	
		115					120					125				
aag	atg	gcc	cgc	gcc	tac	tgg	cgc	ctg	aaa	ggc	cag	ccg	cag	aag	acc	432
Lys	Met	Ala	Arg	Ala	Tyr	Trp	Arg	Leu	Lys	Gly	Gln	Pro	Gln	Lys	Thr	
	130					135					140					
aag	ctg	atc	ggc	cgc	gcc	cgc	ggc	tac	cac	ggg	gtc	aac	gtc	gcc	ggc	480
Lys	Leu	Ile	Gly	Arg	Ala	Arg	Gly	Tyr	His	Gly	Val	Asn	Val	Ala	Gly	
145					150					155					160	
acc	agc	ctc	ggc	ggg	atc	ggg	ggc	aac	cgc	aag	atg	ttc	ggc	cag	ctg	528
Thr	Ser	Leu	Gly	Gly	Ile	Gly	Gly	Asn	Arg	Lys	Met	Phe	Gly	Gln	Leu	
				165				170						175		
atg	gac	gtc	gac	cat	ctg	ccg	cac	acc	ctt	caa	ccg	ggc	atg	gcg	ttc	576
Met	Asp	Val	Asp	His	Leu	Pro	His	Thr	Leu	Gln	Pro	Gly	Met	Ala	Phe	
			180					185					190			
acc	cgc	ggg	atg	gcc	cag	acc	ggc	ggc	gtc	gag	ctg	gcc	aac	gag	ctg	624
Thr	Arg	Gly	Met	Ala	Gln	Thr	Gly	Gly	Val	Glu	Leu	Ala	Asn	Glu	Leu	
		195					200					205				
ctc	aag	ctg	atc	gaa	ctg	cac	gac	gcc	tcg	aac	atc	gcc	gcg	gtg	atc	672
Leu	Lys	Leu	Ile	Glu	Leu	His	Asp	Ala	Ser	Asn	Ile	Ala	Ala	Val	Ile	
	210					215					220					
gtc	gag	ccg	atg	tcc	ggc	tcc	gcc	ggc	gta	ctg	gta	ccg	ccg	gtc	ggc	720
Val	Glu	Pro	Met	Ser	Gly	Ser	Ala	Gly	Val	Leu	Val	Pro	Pro	Val	Gly	
225					230				235					240		
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Tyr	Leu	Gln	Arg	Leu	Arg	Glu	Ile	Cys	Asp	Gln	His	Asn	Ile	Leu	Leu	
				245				250						255		
atc	ttc	gac	gag	gtg	atc	acc	gcc	ttc	ggc	cgc	ctg	ggc	acc	tac	agc	816
Ile	Phe	Asp	Glu	Val	Ile	Thr	Ala	Phe	Gly	Arg	Leu	Gly	Thr	Tyr	Ser	
			260					265					270			
ggc	gcc	gag	tac	ttc	ggc	gtc	acc	ccg	gac	ctg	atg	aac	gtc	gcc	aag	864
Gly	Ala	Glu	Tyr	Phe	Gly	Val	Thr	Pro	Asp	Leu	Met	Asn	Val	Ala	Lys	
		275					280					285				
cag	gtc	acc	aac	ggc	gcc	gtg	ccg	atg	ggc	gcg	gtg	atc	gcc	agc	agc	912
Gln	Val	Thr	Asn	Gly	Ala	Val	Pro	Met	Gly	Ala	Val	Ile	Ala	Ser	Ser	
	290					295					300					
gag	atc	tac	gac	acc	ttc	atg	aac	cag	gcg	ctg	ccc	gag	cac	gcg	gtg	960
Glu	Ile	Tyr	Asp	Thr	Phe	Met	Asn	Gln	Ala	Leu	Pro	Glu	His	Ala	Val	

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305	310	315	320	
gag ttc agc cac ggc tac acc tac tcc gcg cac ccg gtc gcc tgc gcc				1008
Glu Phe Ser His Gly Tyr Thr Tyr Ser Ala His Pro Val Ala Cys Ala				
	325	330	335	
gcc ggc ctc gcc gcg ctg gac atc ctg gcc agg gac aac ctg gtg cag				1056
Ala Gly Leu Ala Ala Leu Asp Ile Leu Ala Arg Asp Asn Leu Val Gln				
	340	345	350	
cag tcc gcc gag ctg gcg ccg cac ttc gag aag ggc ctg cac ggc ctg				1104
Gln Ser Ala Glu Leu Ala Pro His Phe Glu Lys Gly Leu His Gly Leu				
	355	360	365	
caa ggc gcg aag aac gtc atc gac atc cgc aac tgc ggc ctg gcc ggc				1152
Gln Gly Ala Lys Asn Val Ile Asp Ile Arg Asn Cys Gly Leu Ala Gly				
	370	375	380	
gcg atc cag atc gcc ccg cgc gac ggc gat ccg acc gtg cgt ccg ttc				1200
Ala Ile Gln Ile Ala Pro Arg Asp Gly Asp Pro Thr Val Arg Pro Phe				
	385	390	395	400
gag gcc ggc atg aag ctc tgg caa cag ggt ttc tac gtg cgc ttc ggc				1248
Glu Ala Gly Met Lys Leu Trp Gln Gln Gly Phe Tyr Val Arg Phe Gly				
	405	410	415	
ggc gat acc ctg caa ttc ggc ccg acc ttc aac gcc agg ccg gaa gag				1296
Gly Asp Thr Leu Gln Phe Gly Pro Thr Phe Asn Ala Arg Pro Glu Glu				
	420	425	430	
ctg gac cgc ctg ttc gac gcg gtc ggc gaa gcg ctc aac ggc atc gcc				1344
Leu Asp Arg Leu Phe Asp Ala Val Gly Glu Ala Leu Asn Gly Ile Ala				
	435	440	445	
tga				1347

&lt;210&gt; 20

&lt;211&gt; 448

&lt;212&gt; PRT

&lt;213&gt; Pseudomonas aeruginosa

&lt;400&gt; 20

Met	Asn	Gln	Pro	Leu	Asn	Val	Ala	Pro	Pro	Val	Ser	Ser	Glu	Leu	Asn
1				5					10					15	

Leu	Arg	Ala	His	Trp	Met	Pro	Phe	Ser	Ala	Asn	Arg	Asn	Phe	Gln	Lys
			20					25					30		

Asp	Pro	Arg	Ile	Ile	Val	Ala	Ala	Glu	Gly	Ser	Trp	Leu	Thr	Asp	Asp
		35					40					45			

Lys	Gly	Arg	Lys	Val	Tyr	Asp	Ser	Leu	Ser	Gly	Leu	Trp	Thr	Cys	Gly
	50					55					60				

Ala	Gly	His	Ser	Arg	Lys	Glu	Ile	Gln	Glu	Ala	Val	Ala	Arg	Gln	Leu
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65		70		75		80
Gly Thr Leu Asp Tyr Ser Pro Gly Phe Gln Tyr Gly His Pro Leu Ser	85		90		95	
Phe Gln Leu Ala Glu Lys Ile Ala Gly Leu Leu Pro Gly Glu Leu Asn	100		105		110	
His Val Phe Phe Thr Gly Ser Gly Ser Glu Cys Ala Asp Thr Ser Ile	115		120		125	
Lys Met Ala Arg Ala Tyr Trp Arg Leu Lys Gly Gln Pro Gln Lys Thr	130		135		140	
Lys Leu Ile Gly Arg Ala Arg Gly Tyr His Gly Val Asn Val Ala Gly	145		150		155	160
Thr Ser Leu Gly Gly Ile Gly Gly Asn Arg Lys Met Phe Gly Gln Leu		165		170		175
Met Asp Val Asp His Leu Pro His Thr Leu Gln Pro Gly Met Ala Phe		180		185		190
Thr Arg Gly Met Ala Gln Thr Gly Gly Val Glu Leu Ala Asn Glu Leu		195		200		205
Leu Lys Leu Ile Glu Leu His Asp Ala Ser Asn Ile Ala Ala Val Ile		210		215		220
Val Glu Pro Met Ser Gly Ser Ala Gly Val Leu Val Pro Pro Val Gly		225		230		235
Tyr Leu Gln Arg Leu Arg Glu Ile Cys Asp Gln His Asn Ile Leu Leu		245		250		255
Ile Phe Asp Glu Val Ile Thr Ala Phe Gly Arg Leu Gly Thr Tyr Ser		260		265		270
Gly Ala Glu Tyr Phe Gly Val Thr Pro Asp Leu Met Asn Val Ala Lys		275		280		285
Gln Val Thr Asn Gly Ala Val Pro Met Gly Ala Val Ile Ala Ser Ser		290		295		300
Glu Ile Tyr Asp Thr Phe Met Asn Gln Ala Leu Pro Glu His Ala Val		305		310		315
						320

Glu Phe Ser His Gly Tyr Thr Tyr Ser Ala His Pro Val Ala Cys Ala  
325 330 335

Ala Gly Leu Ala Ala Leu Asp Ile Leu Ala Arg Asp Asn Leu Val Gln  
340 345 350

Gln Ser Ala Glu Leu Ala Pro His Phe Glu Lys Gly Leu His Gly Leu  
355 360 365

Gln Gly Ala Lys Asn Val Ile Asp Ile Arg Asn Cys Gly Leu Ala Gly  
370 375 380

Ala Ile Gln Ile Ala Pro Arg Asp Gly Asp Pro Thr Val Arg Pro Phe  
385 390 395 400

Glu Ala Gly Met Lys Leu Trp Gln Gln Gly Phe Tyr Val Arg Phe Gly  
405 410 415

Gly Asp Thr Leu Gln Phe Gly Pro Thr Phe Asn Ala Arg Pro Glu Glu  
420 425 430

Leu Asp Arg Leu Phe Asp Ala Val Gly Glu Ala Leu Asn Gly Ile Ala  
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<210> 21
<211> 1416
<212> DNA
<213> Bacillus subtilis
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<222> (1) .. (1413)
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Met Lys Asn Lys Trp Tyr Lys Pro Lys Arg His Trp Lys Glu Ile Glu
1           5           10           15
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tta	tgg	aag	gac	gtt	ccg	gaa	gag	aaa	tgg	aac	gat	tgg	ctt	tgg	cag	96
Leu	Trp	Lys	Asp	Val	Pro	Glu	Glu	Lys	Trp	Asn	Asp	Trp	Leu	Trp	Gln	
		20						25					30			

ctg aca cac act gta aga acg tta gat gat tta aag aaa gtc att aat 144  
Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn  
35 40 45

ctg acc gag gat gaa gag gaa ggc gtc cgt att tct acc aaa acg atc 192  
Leu Thr Glu Asp Glu Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile  
50 55 60

ccc tta aat att aca cct tac tat gct tct tta atg gac ccc gac aat Pro Leu Asn Ile Thr Pro Tyr Tyr Ala Ser Leu Met Asp Pro Asp Asn 65 70 75 80	240
ccg aga tgc ccg gta cgc atg cag tct gtg ccg ctt tct gaa gaa atg Pro Arg Cys Pro Val Arg Met Gln Ser Val Pro Leu Ser Glu Glu Met 85 90 95	288
cac aaa aca aaa tac gat atg gaa gac ccg ctt cat gag gat gaa gat His Lys Thr Lys Tyr Asp Met Glu Asp Pro Leu His Glu Asp Glu Asp 100 105 110	336
tca ccg gta ccc ggt ctg aca cac cgc tat ccc gac cgt gtg ctg ttt Ser Pro Val Pro Gly Leu Thr His Arg Tyr Pro Asp Arg Val Leu Phe 115 120 125	384
ctt gtc acg aat caa tgt tcc gtg tac tgc cgc cac tgc aca cgc cgg Leu Val Thr Asn Gln Cys Ser Val Tyr Cys Arg His Cys Thr Arg Arg 130 135 140	432
cgc ttt tcc gga caa atc gga atg ggc gtc ccc aaa aaa cag ctt gat Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp 145 150 155 160	480
gct gca att gct tat atc cgg gaa aca ccc gaa atc cgc gat tgt tta Ala Ala Ile Ala Tyr Ile Arg Glu Thr Pro Glu Ile Arg Asp Cys Leu 165 170 175	528
att tca ggc ggt gat ggg ctg ctc atc aac gac caa att tta gaa tat Ile Ser Gly Gly Asp Gly Leu Leu Ile Asn Asp Gln Ile Leu Glu Tyr 180 185 190	576
att tta aaa gag ctg cgc agc att ccg cat ctg gaa gtc atc cgc atc Ile Leu Lys Glu Leu Arg Ser Ile Pro His Leu Glu Val Ile Arg Ile 195 200 205	624
gga aca cgt gct ccc gtc gtc ttt ccg cag cgc att acc gat cat ctg Gly Thr Arg Ala Pro Val Val Phe Pro Gln Arg Ile Thr Asp His Leu 210 215 220	672
tgc gag ata ttg aaa aaa tat cat ccg gtc tgg ctg aac acc cat ttt Cys Glu Ile Leu Lys Lys Tyr His Pro Val Trp Leu Asn Thr His Phe 225 230 235 240	720
aac aca agc atc gaa atg aca gaa gaa tcc gtt gag gca tgt gaa aag Asn Thr Ser Ile Glu Met Thr Glu Glu Ser Val Glu Ala Cys Glu Lys 245 250 255	768
ctg gtg aac gcg gga gtg ccg gtc gga aat cag gct gtc gta tta gca Leu Val Asn Ala Gly Val Pro Val Gly Asn Gln Ala Val Val Leu Ala 260 265 270	816
ggt att aat gat tcg gtt cca att atg aaa aag ctc atg cat gac ttg Gly Ile Asn Asp Ser Val Pro Ile Met Lys Lys Leu Met His Asp Leu 275 280 285	864
gta aaa atc aga gtc cgt cct tat tat att tac caa tgt gat ctg tca Val Lys Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Ser 290 295 300	912
gaa gga ata ggg cat ttc cgt gct cct gtt tcc aaa ggt ttg gag atc	960

Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile  
 305 310 315 320  
 att gaa ggg ctg aga ggt cat acc tca ggc tat gcg gtt cct acc ttt 1008  
 Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe  
 325 330 335  
 gtc gtt cac gca cca ggc gga gga ggt aaa atc gcc ctg cag ccg aac 1056  
 Val Val His Ala Pro Gly Gly Gly Lys Ile Ala Leu Gln Pro Asn  
 340 345 350  
 tat gtc ctg tca caa agt cct gac aaa gtg atc tta aga aat ttt gaa 1104  
 Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu  
 355 360 365  
 ggt gtg att acg tca tat ccg gaa cca gag aat tat atc ccc aat cag 1152  
 Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln  
 370 375 380  
 gca gac gcc tat ttt gag tcc gtt ttc cct gaa acc gct gac aaa aag 1200  
 Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys  
 385 390 395 400  
 gag ccg atc ggg ctg agt gcc att ttt gct gac aaa gaa gtt tcg ttt 1248  
 Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe  
 405 410 415  
 aca cct gaa aat gta gac aga atc aaa cgg cgt gag gca tac atc gca 1296  
 Thr Pro Glu Asn Val Asp Arg Ile Lys Arg Arg Glu Ala Tyr Ile Ala  
 420 425 430  
 aat ccg gag cat gaa aca tta aaa gat cgg cgt gag aaa aga gat cag 1344  
 Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln  
 435 440 445  
 ctc aaa gaa aag aaa ttt ttg gcg cag cag aaa aaa cag aaa gag act 1392  
 Leu Lys Glu Lys Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr  
 450 455 460  
 gaa tgc gga ggg gat tct tca tga 1416  
 Glu Cys Gly Gly Asp Ser Ser  
 465 470

&lt;210&gt; 22

&lt;211&gt; 471

&lt;212&gt; PRT

<213> *Bacillus subtilis*

&lt;400&gt; 22

Met Lys Asn Lys Trp Tyr Lys Pro Lys Arg His Trp Lys Glu Ile Glu  
 1 5 10 15

Leu Trp Lys Asp Val Pro Glu Glu Lys Trp Asn Asp Trp Leu Trp Gln  
 20 25 30

Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn  
 35 40 45

Leu Thr Glu Asp Glu Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile  
 50 55 60

Pro Leu Asn Ile Thr Pro Tyr Tyr Ala Ser Leu Met Asp Pro Asp Asn  
 65 70 75 80

Pro Arg Cys Pro Val Arg Met Gln Ser Val Pro Leu Ser Glu Glu Met  
 85 90 95

His Lys Thr Lys Tyr Asp Met Glu Asp Pro Leu His Glu Asp Glu Asp  
 100 105 110

Ser Pro Val Pro Gly Leu Thr His Arg Tyr Pro Asp Arg Val Leu Phe  
 115 120 125

Leu Val Thr Asn Gln Cys Ser Val Tyr Cys Arg His Cys Thr Arg Arg  
 130 135 140

Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp  
 145 150 155 160

Ala Ala Ile Ala Tyr Ile Arg Glu Thr Pro Glu Ile Arg Asp Cys Leu  
 165 170 175

Ile Ser Gly Gly Asp Gly Leu Leu Ile Asn Asp Gln Ile Leu Glu Tyr  
 180 185 190

Ile Leu Lys Glu Leu Arg Ser Ile Pro His Leu Glu Val Ile Arg Ile  
 195 200 205

Gly Thr Arg Ala Pro Val Val Phe Pro Gln Arg Ile Thr Asp His Leu  
 210 215 220

Cys Glu Ile Leu Lys Lys Tyr His Pro Val Trp Leu Asn Thr His Phe  
 225 230 235 240

Asn Thr Ser Ile Glu Met Thr Glu Glu Ser Val Glu Ala Cys Glu Lys  
 245 250 255

Leu Val Asn Ala Gly Val Pro Val Gly Asn Gln Ala Val Val Leu Ala  
 260 265 270

Gly Ile Asn Asp Ser Val Pro Ile Met Lys Lys Leu Met His Asp Leu  
 275 280 285

Val Lys Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Ser  
 290 295 300

Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile  
 305 310 315 320

Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe  
 325 330 335

Val Val His Ala Pro Gly Gly Gly Gly Lys Ile Ala Leu Gln Pro Asn  
 340 345 350

Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu  
 355 360 365

Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln  
 370 375 380

Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys  
 385 390 395 400

Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe  
 405 410 415

Thr Pro Glu Asn Val Asp Arg Ile Lys Arg Arg Glu Ala Tyr Ile Ala  
 420 425 430

Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln  
 435 440 445

Leu Lys Glu Lys Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr  
 450 455 460

Glu Cys Gly Gly Asp Ser Ser  
 465 470

<210> 23  
 <211> 1416  
 <212> DNA  
 <213> Bacillus subtilis

<220>  
 <221> CDS  
 <222> (1) .. (1413)

<400> 23  
 atg aaa aac aaa tgg tat aaa ccg aaa cgg cat tgg aag gag atc gag



Met	Lys	Asn	Lys	Trp	Tyr	Lys	Pro	Lys	Arg	His	Trp	Lys	Glu	Ile	Glu		
1				5					10					15			
tta	tgg	aag	gac	gtt	ccg	gaa	gag	aaa	tgg	aac	gat	tgg	ctt	tgg	cag		96
Leu	Trp	Lys	Asp	Val	Pro	Glu	Glu	Lys	Trp	Asn	Asp	Trp	Leu	Trp	Gln		
			20					25					30				
ctg	aca	cac	act	gta	aga	acg	tta	gat	gat	tta	aag	aaa	gtc	att	aat		144
Leu	Thr	His	Thr	Val	Arg	Thr	Leu	Asp	Asp	Leu	Lys	Lys	Val	Ile	Asn		
			35				40					45					
ctg	acc	gag	gat	gaa	gag	gaa	ggc	gtc	aga	att	tct	acc	aaa	acg	atc		192
Leu	Thr	Glu	Asp	Glu	Glu	Glu	Gly	Val	Arg	Ile	Ser	Thr	Lys	Thr	Ile		
	50					55					60						
ccc	tta	aat	att	aca	cct	tac	tat	gct	tct	tta	atg	gac	ccc	gac	aat		240
Pro	Leu	Asn	Ile	Thr	Pro	Tyr	Tyr	Ala	Ser	Leu	Met	Asp	Pro	Asp	Asn		
65					70				75						80		
ccg	aga	tgc	ccg	gta	cgc	atg	cag	tct	gtg	ccg	ctt	tct	gaa	gaa	atg		288
Pro	Arg	Cys	Pro	Val	Arg	Met	Gln	Ser	Val	Pro	Leu	Ser	Glu	Glu	Met		
				85				90						95			
cac	aaa	aca	aaa	tac	gat	atg	gaa	gac	ccg	ctt	cat	gag	gat	gaa	gat		336
His	Lys	Thr	Lys	Tyr	Asp	Met	Glu	Asp	Pro	Leu	His	Glu	Asp	Glu	Asp		
			100					105					110				
tca	ccg	gta	ccc	ggg	ctg	aca	cac	cgc	tat	ccc	gac	cgt	gtg	ctg	ttt		384
Ser	Pro	Val	Pro	Gly	Leu	Thr	His	Arg	Tyr	Pro	Asp	Arg	Val	Leu	Phe		
		115					120					125					
ctt	gtc	acg	aat	caa	tgt	tcc	gtg	tac	tgc	cgc	tac	tgc	aca	aga	agg		432
Leu	Val	Thr	Asn	Gln	Cys	Ser	Val	Tyr	Cys	Arg	Tyr	Cys	Thr	Arg	Arg		
	130					135					140						
cgc	ttt	tcc	gga	caa	atc	gga	atg	ggc	gtc	ccc	aaa	aaa	cag	ctt	gat		480
Arg	Phe	Ser	Gly	Gln	Ile	Gly	Met	Gly	Val	Pro	Lys	Lys	Gln	Leu	Asp		
145					150					155					160		
gct	gca	att	gct	tat	atc	cgg	gaa	aca	ccc	gaa	atc	cgc	gat	tgt	tta		528
Ala	Ala	Ile	Ala	Tyr	Ile	Arg	Glu	Thr	Pro	Glu	Ile	Arg	Asp	Cys	Leu		
				165					170					175			
att	tca	ggc	ggg	gat	ggg	ctg	ctc	atc	aac	gac	caa	att	tta	gaa	tat		576
Ile	Ser	Gly	Gly	Asp	Gly	Leu	Leu	Ile	Asn	Asp	Gln	Ile	Leu	Glu	Tyr		
			180					185					190				
att	tta	aaa	gag	ctg	cgc	agc	att	ccg	cat	ctg	gaa	gtc	atc	aga	atc		624
Ile	Leu	Lys	Glu	Leu	Arg	Ser	Ile	Pro	His	Leu	Glu	Val	Ile	Arg	Ile		
		195					200					205					
gga	aca	aga	gct	ccc	gtc	gtc	ttt	ccg	cag	cgc	att	acc	gat	cat	ctg		672
Gly	Thr	Arg	Ala	Pro	Val	Val	Phe	Pro	Gln	Arg	Ile	Thr	Asp	His	Leu		
	210					215					220						
tgc	gag	ata	ttg	aaa	aaa	tat	cat	ccg	gtc	tgg	ctg	aac	acc	cat	ttt		720
Cys	Glu	Ile	Leu	Lys	Lys	Tyr	His	Pro	Val	Trp	Leu	Asn	Thr	His	Phe		
225					230					235					240		
aac	aca	agc	atc	gaa	atg	aca	gaa	gaa	tcc	gtt	gag	gca	tgt	gaa	aag		768
Asn	Thr	Ser	Ile	Glu	Met	Thr	Glu	Glu	Ser	Val	Glu	Ala	Cys	Glu	Lys		

245								250					255					
ctg	gtg	aac	gcg	gga	gtg	ccg	gtc	gga	aat	cag	gct	gtc	gta	tta	gca	816		
Leu	Val	Asn	Ala	Gly	Val	Pro	Val	Gly	Asn	Gln	Ala	Val	Val	Leu	Ala			
			260					265					270					
ggg	att	aat	gat	tcg	gtt	cca	att	atg	aaa	aag	ctc	atg	cat	gac	ttg	864		
Gly	Ile	Asn	Asp	Ser	Val	Pro	Ile	Met	Lys	Lys	Leu	Met	His	Asp	Leu			
		275					280					285						
gta	aaa	atc	aga	gtc	cgt	cct	tat	tat	att	tac	caa	tgt	gat	ctg	tca	912		
Val	Lys	Ile	Arg	Val	Arg	Pro	Tyr	Tyr	Ile	Tyr	Gln	Cys	Asp	Leu	Ser			
	290					295					300							
gaa	gga	ata	ggg	cat	ttc	aga	gct	cct	gtt	tcc	aaa	ggg	ttg	gag	atc	960		
Glu	Gly	Ile	Gly	His	Phe	Arg	Ala	Pro	Val	Ser	Lys	Gly	Leu	Glu	Ile			
305					310					315					320			
att	gaa	ggg	ctg	aga	ggg	cat	acc	tca	ggc	tat	gcg	gtt	cct	acc	ttt	1008		
Ile	Glu	Gly	Leu	Arg	Gly	His	Thr	Ser	Gly	Tyr	Ala	Val	Pro	Thr	Phe			
				325					330					335				
gtc	gtt	cac	gca	cca	ggc	gga	gga	ggg	aaa	atc	gcc	ctg	cag	ccg	aac	1056		
Val	Val	His	Ala	Pro	Gly	Gly	Gly	Gly	Lys	Ile	Ala	Leu	Gln	Pro	Asn			
			340					345					350					
tat	gtc	ctg	tca	caa	agt	cct	gac	aaa	gtg	atc	tta	aga	aat	ttt	gaa	1104		
Tyr	Val	Leu	Ser	Gln	Ser	Pro	Asp	Lys	Val	Ile	Leu	Arg	Asn	Phe	Glu			
		355					360					365						
ggg	gtg	att	acg	tca	tat	ccg	gaa	cca	gag	aat	tat	atc	ccc	aat	cag	1152		
Gly	Val	Ile	Thr	Ser	Tyr	Pro	Glu	Pro	Glu	Asn	Tyr	Ile	Pro	Asn	Gln			
	370					375					380							
gca	gac	gcc	tat	ttt	gag	tcc	gtt	ttc	cct	gaa	acc	gct	gac	aaa	aag	1200		
Ala	Asp	Ala	Tyr	Phe	Glu	Ser	Val	Phe	Pro	Glu	Thr	Ala	Asp	Lys	Lys			
385					390					395					400			
gag	ccg	atc	ggg	ctg	agt	gcc	att	ttt	gct	gac	aaa	gaa	gtt	tcg	ttt	1248		
Glu	Pro	Ile	Gly	Leu	Ser	Ala	Ile	Phe	Ala	Asp	Lys	Glu	Val	Ser	Phe			
			405						410					415				
aca	cct	gaa	aat	gta	gac	aga	atc	aaa	agg	aga	gag	gca	tac	atc	gca	1296		
Thr	Pro	Glu	Asn	Val	Asp	Arg	Ile	Lys	Arg	Arg	Glu	Ala	Tyr	Ile	Ala			
			420					425					430					
aat	ccg	gag	cat	gaa	aca	tta	aaa	gat	cgg	cgt	gag	aaa	aga	gat	cag	1344		
Asn	Pro	Glu	His	Glu	Thr	Leu	Lys	Asp	Arg	Arg	Glu	Lys	Arg	Asp	Gln			
		435					440				445							
ctc	aaa	gaa	aag	aaa	ttt	ttg	gcg	cag	cag	aaa	aaa	cag	aaa	gag	act	1392		
Leu	Lys	Glu	Lys	Lys	Phe	Leu	Ala	Gln	Gln	Lys	Lys	Gln	Lys	Glu	Thr			
	450					455					460							
gaa	tgc	gga	ggg	gat	tct	tca	tga									1416		
Glu	Cys	Gly	Gly	Asp	Ser	Ser												
465					470													

&lt;210&gt; 24

&lt;211&gt; 471

19/27

&lt;212&gt; PRT

&lt;213&gt; Bacillus subtilis

&lt;400&gt; 24

Met Lys Asn Lys Trp Tyr Lys Pro Lys Arg His Trp Lys Glu Ile Glu  
1 5 10 15

Leu Trp Lys Asp Val Pro Glu Glu Lys Trp Asn Asp Trp Leu Trp Gln  
20 25 30

Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn  
35 40 45

Leu Thr Glu Asp Glu Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile  
50 55 60

Pro Leu Asn Ile Thr Pro Tyr Tyr Ala Ser Leu Met Asp Pro Asp Asn  
65 70 75 80

Pro Arg Cys Pro Val Arg Met Gln Ser Val Pro Leu Ser Glu Glu Met  
85 90 95

His Lys Thr Lys Tyr Asp Met Glu Asp Pro Leu His Glu Asp Glu Asp  
100 105 110

Ser Pro Val Pro Gly Leu Thr His Arg Tyr Pro Asp Arg Val Leu Phe  
115 120 125

Leu Val Thr Asn Gln Cys Ser Val Tyr Cys Arg Tyr Cys Thr Arg Arg  
130 135 140

Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp  
145 150 155 160

Ala Ala Ile Ala Tyr Ile Arg Glu Thr Pro Glu Ile Arg Asp Cys Leu  
165 170 175

Ile Ser Gly Gly Asp Gly Leu Leu Ile Asn Asp Gln Ile Leu Glu Tyr  
180 185 190

Ile Leu Lys Glu Leu Arg Ser Ile Pro His Leu Glu Val Ile Arg Ile  
195 200 205

Gly Thr Arg Ala Pro Val Val Phe Pro Gln Arg Ile Thr Asp His Leu  
210 215 220

Cys Glu Ile Leu Lys Lys Tyr His Pro Val Trp Leu Asn Thr His Phe  
225 230 235 240

Asn Thr Ser Ile Glu Met Thr Glu Glu Ser Val Glu Ala Cys Glu Lys  
245 250 255

Leu Val Asn Ala Gly Val Pro Val Gly Asn Gln Ala Val Val Leu Ala  
260 265 270

Gly Ile Asn Asp Ser Val Pro Ile Met Lys Lys Leu Met His Asp Leu  
275 280 285

Val Lys Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Ser  
290 295 300

Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile  
305 310 315 320

Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe  
325 330 335

Val Val His Ala Pro Gly Gly Gly Gly Lys Ile Ala Leu Gln Pro Asn  
340 345 350

Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu  
355 360 365

Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln  
370 375 380

Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys  
385 390 395 400

Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe  
405 410 415

Thr Pro Glu Asn Val Asp Arg Ile Lys Arg Arg Glu Ala Tyr Ile Ala  
420 425 430

Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln  
435 440 445

Leu Lys Glu Lys Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr  
450 455 460

Glu Cys Gly Gly Asp Ser Ser

465

470

<210> 25  
 <211> 1251  
 <212> DNA  
 <213> Porphyromonas gingivalis

<220>  
 <221> CDS  
 <222> (1)..(1248)

<400> 25  
 atg gca gaa agt cgt aga aag tat tat ttc cct gat gtc acc gat gag 48  
 Met Ala Glu Ser Arg Arg Lys Tyr Tyr Phe Pro Asp Val Thr Asp Glu  
 1 5 10 15

caa tgg tac gac tgg cat tgg cag gtc ctc aat cga att gag acg ctc 96  
 Gln Trp Tyr Asp Trp His Trp Gln Val Leu Asn Arg Ile Glu Thr Leu  
 20 25 30

gac cag ctg aaa aag tac gtt aca ctc acc gct gaa gaa gaa gag gga 144  
 Asp Gln Leu Lys Lys Tyr Val Thr Leu Thr Ala Glu Glu Glu Glu Gly  
 35 40 45

gta aaa gaa tcg ccc aaa gta ctc cga atg gct atc aca cct tat tat 192  
 Val Lys Glu Ser Pro Lys Val Leu Arg Met Ala Ile Thr Pro Tyr Tyr  
 50 55 60

ttg agt ttg ata gac ccc gag aat cct aat tgt ccg att cgt aaa caa 240  
 Leu Ser Leu Ile Asp Pro Glu Asn Pro Asn Cys Pro Ile Arg Lys Gln  
 65 70 75 80

gcc att cct act caa cag gaa ctg gta cgt gct cct gaa gat cag gta 288  
 Ala Ile Pro Thr Gln Gln Glu Leu Val Arg Ala Pro Glu Asp Gln Val  
 85 90 95

gac cca ctt agt gaa gat gaa gat tcg ccc gta ccc gga ctg act cat 336  
 Asp Pro Leu Ser Glu Asp Glu Asp Ser Pro Val Pro Gly Leu Thr His  
 100 105 110

cgt tat ccg gat cgt gta ttg ttc ctt atc acg gac aaa tgt tcg atg 384  
 Arg Tyr Pro Asp Arg Val Leu Phe Leu Ile Thr Asp Lys Cys Ser Met  
 115 120 125

tac tgt cgt cat tgt act cgc cgt cgc ttc gca gga cag aaa gat gct 432  
 Tyr Cys Arg His Cys Thr Arg Arg Arg Phe Ala Gly Gln Lys Asp Ala  
 130 135 140

tct tct cct tct gag cgc atc gat cga tgc att gac tat ata gcc aat 480  
 Ser Ser Pro Ser Glu Arg Ile Asp Arg Cys Ile Asp Tyr Ile Ala Asn  
 145 150 155 160

aca ccg aca gtc cgc gat gtt ttg cta tcg gga ggc gat gcc ctc ctt 528  
 Thr Pro Thr Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu  
 165 170 175

gtc agc gac gaa cgc ttg gaa tac ata ttg aag cgt ctg cgc gaa ata 576  
 Val Ser Asp Glu Arg Leu Glu Tyr Ile Leu Lys Arg Leu Arg Glu Ile  
 180 185 190

cct cat gtg gag att gtt cgt ata gga agc cgt acg ccg gta gtc ctc Pro His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu 195 200 205	624
cct cag cgt ata acg cct caa ttg gtg gat atg ctc aaa aaa tat cat Pro Gln Arg Ile Thr Pro Gln Leu Val Asp Met Leu Lys Lys Tyr His 210 215 220	672
ccg gtg tgg ctg aac act cac ttc aac cac ccg aat gaa gtt acc gaa Pro Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Val Thr Glu 225 230 235 240	720
gaa gca gta gag gct tgt gaa aga atg gcc aat gcc ggt att ccg ttg Glu Ala Val Glu Ala Cys Glu Arg Met Ala Asn Ala Gly Ile Pro Leu 245 250 255	768
ggc aac caa acg gtt tta ttg cgt gga atc aat gat tgt aca cat gtg Gly Asn Gln Thr Val Leu Leu Arg Gly Ile Asn Asp Cys Thr His Val 260 265 270	816
atg aag aga ttg gta cat ttg ctg gta aag atg cgt gtg cgt cct tac Met Lys Arg Leu Val His Leu Leu Val Lys Met Arg Val Arg Pro Tyr 275 280 285	864
tat ata tat gta tgc gat ctt tcg ctt gga ata ggt cat ttc cgc acg Tyr Ile Tyr Val Cys Asp Leu Ser Leu Gly Ile Gly His Phe Arg Thr 290 295 300	912
ccg gta tct aaa gga atc gaa att atc gaa aat ttg cgc gga cac acc Pro Val Ser Lys Gly Ile Glu Ile Ile Glu Asn Leu Arg Gly His Thr 305 310 315 320	960
tcg ggc tat gca gtt cct acc ttt gtg gta ggt gct ccg ggg ggt ggt Ser Gly Tyr Ala Val Pro Thr Phe Val Val Gly Ala Pro Gly Gly Gly 325 330 335	1008
ggc aag ata cct gta acg ccg aac tat gtt gta tct cag tcc cca cga Gly Lys Ile Pro Val Thr Pro Asn Tyr Val Val Ser Gln Ser Pro Arg 340 345 350	1056
cat gtg gtt ctt cgc aat tat gaa ggt gtt atc aca acc tat acg gag His Val Val Leu Arg Asn Tyr Glu Gly Val Ile Thr Thr Tyr Thr Glu 355 360 365	1104
ccg gag aat tat cat gag gag tgc gat tgt gag gac tgt cga gcc ggt Pro Glu Asn Tyr His Glu Glu Cys Asp Cys Glu Asp Cys Arg Ala Gly 370 375 380	1152
aag cat aaa gag ggt gta gct gca ctt tcc gga ggt cag cag ttg gct Lys His Lys Glu Gly Val Ala Ala Leu Ser Gly Gly Gln Gln Leu Ala 385 390 395 400	1200
atc gag cct tcc gac tta gct cgc aaa aaa cgc aag ttt gat aag aac Ile Glu Pro Ser Asp Leu Ala Arg Lys Lys Arg Lys Phe Asp Lys Asn 405 410 415	1248
tga	1251

&lt;211&gt; 416

&lt;212&gt; PRT

&lt;213&gt; Porphyromonas gingivalis

&lt;400&gt; 26

Met Ala Glu Ser Arg Arg Lys Tyr Tyr Phe Pro Asp Val Thr Asp Glu  
 1 5 10 15

Gln Trp Tyr Asp Trp His Trp Gln Val Leu Asn Arg Ile Glu Thr Leu  
 20 25 30

Asp Gln Leu Lys Lys Tyr Val Thr Leu Thr Ala Glu Glu Glu Gly  
 35 40 45

Val Lys Glu Ser Pro Lys Val Leu Arg Met Ala Ile Thr Pro Tyr Tyr  
 50 55 60

Leu Ser Leu Ile Asp Pro Glu Asn Pro Asn Cys Pro Ile Arg Lys Gln  
 65 70 75 80

Ala Ile Pro Thr Gln Gln Glu Leu Val Arg Ala Pro Glu Asp Gln Val  
 85 90 95

Asp Pro Leu Ser Glu Asp Glu Asp Ser Pro Val Pro Gly Leu Thr His  
 100 105 110

Arg Tyr Pro Asp Arg Val Leu Phe Leu Ile Thr Asp Lys Cys Ser Met  
 115 120 125

Tyr Cys Arg His Cys Thr Arg Arg Arg Phe Ala Gly Gln Lys Asp Ala  
 130 135 140

Ser Ser Pro Ser Glu Arg Ile Asp Arg Cys Ile Asp Tyr Ile Ala Asn  
 145 150 155 160

Thr Pro Thr Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu  
 165 170 175

Val Ser Asp Glu Arg Leu Glu Tyr Ile Leu Lys Arg Leu Arg Glu Ile  
 180 185 190

Pro His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu  
 195 200 205

Pro Gln Arg Ile Thr Pro Gln Leu Val Asp Met Leu Lys Lys Tyr His  
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Pro Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Val Thr Glu  
225 230 235 240

Glu Ala Val Glu Ala Cys Glu Arg Met Ala Asn Ala Gly Ile Pro Leu  
245 250 255

Gly Asn Gln Thr Val Leu Leu Arg Gly Ile Asn Asp Cys Thr His Val  
260 265 270

Met Lys Arg Leu Val His Leu Leu Val Lys Met Arg Val Arg Pro Tyr  
275 280 285

Tyr Ile Tyr Val Cys Asp Leu Ser Leu Gly Ile Gly His Phe Arg Thr  
290 295 300

Pro Val Ser Lys Gly Ile Glu Ile Ile Glu Asn Leu Arg Gly His Thr  
305 310 315 320

Ser Gly Tyr Ala Val Pro Thr Phe Val Val Gly Ala Pro Gly Gly Gly  
325 330 335

Gly Lys Ile Pro Val Thr Pro Asn Tyr Val Val Ser Gln Ser Pro Arg  
340 345 350

His Val Val Leu Arg Asn Tyr Glu Gly Val Ile Thr Thr Tyr Thr Glu  
355 360 365

Pro Glu Asn Tyr His Glu Glu Cys Asp Cys Glu Asp Cys Arg Ala Gly  
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Lys His Lys Glu Gly Val Ala Ala Leu Ser Gly Gly Gln Gln Leu Ala  
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Ala	Ala	Asn	Leu	Leu	Lys	Ala	Gly	His	Arg	Val	Asn	Val	Phe	Asp	Leu	
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cag	ccc	aag	gcc	gtg	ctg	ggc	ctg	gtc	gag	cag	ggc	gcg	cag	ggc	gcc	144
Gln	Pro	Lys	Ala	Val	Leu	Gly	Leu	Val	Glu	Gln	Gly	Ala	Gln	Gly	Ala	
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gat	agc	gcc	ttg	cag	tgc	tgc	gaa	ggc	gcc	gaa	gtg	gtg	atc	agc	atg	192
Asp	Ser	Ala	Leu	Gln	Cys	Cys	Glu	Gly	Ala	Glu	Val	Val	Ile	Ser	Met	
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ctg	ccg	gcc	ggg	cag	cac	gtg	gaa	agc	ctg	tat	ctc	ggc	gac	gac	ggc	240
Leu	Pro	Ala	Gly	Gln	His	Val	Glu	Ser	Leu	Tyr	Leu	Gly	Asp	Asp	Gly	
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ctg	ctc	gcg	cgg	gtc	gcc	ggc	aag	ccc	ctg	ctg	atc	gac	tgc	tcg	acc	288
Leu	Leu	Ala	Arg	Val	Ala	Gly	Lys	Pro	Leu	Leu	Ile	Asp	Cys	Ser	Thr	
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atc	gcc	ccg	gag	acc	gcg	cgc	aag	gtc	gcc	gag	gcc	gcc	gcg	gcg	aag	336
Ile	Ala	Pro	Glu	Thr	Ala	Arg	Lys	Val	Ala	Glu	Ala	Ala	Ala	Ala	Lys	
			100					105					110			
ggc	ctg	acc	ctg	ctc	gac	gcg	ccg	gtt	tcc	ggc	ggc	gtc	ggc	ggc	gcc	384
Gly	Leu	Thr	Leu	Leu	Asp	Ala	Pro	Val	Ser	Gly	Gly	Val	Gly	Gly	Ala	
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cgc	gcc	ggc	acc	ctg	agc	ttc	atc	gtc	ggc	ggc	ccc	gcc	gaa	ggc	ttc	432
Arg	Ala	Gly	Thr	Leu	Ser	Phe	Ile	Val	Gly	Gly	Pro	Ala	Glu	Gly	Phe	
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gcg	cgg	gcc	cgg	ccg	gtc	ctc	gag	aac	atg	ggc	cgg	aac	atc	ttc	cac	480
Ala	Arg	Ala	Arg	Pro	Val	Leu	Glu	Asn	Met	Gly	Arg	Asn	Ile	Phe	His	
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gcc	ggc	gat	cac	ggc	gcc	ggc	cag	gtg	gcg	aag	atc	tgc	aac	aac	atg	528
Ala	Gly	Asp	His	Gly	Ala	Gly	Gln	Val	Ala	Lys	Ile	Cys	Asn	Asn	Met	
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ctc	ctc	ggc	atc	ctc	atg	gcc	ggc	acc	gcc	gag	gcc	ctg	gcg	ctg	ggg	576
Leu	Leu	Gly	Ile	Leu	Met	Ala	Gly	Thr	Ala	Glu	Ala	Leu	Ala	Leu	Gly	
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gtg	aag	aac	ggc	ctc	gac	ccg	gcg	gtg	ctg	tcc	gag	gtg	atg	aag	cag	624
Val	Lys	Asn	Gly	Leu	Asp	Pro	Ala	Val	Leu	Ser	Glu	Val	Met	Lys	Gln	
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Ser	Ser	Gly	Gly	Asn	Trp	Ala	Leu	Asn	Leu	Tyr	Asn	Pro	Trp	Pro	Gly	
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Val	Met	Pro	Gln	Ala	Pro	Ala	Ser	Asn	Gly	Tyr	Ala	Gly	Gly	Phe	Gln	
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gtg	cgc	ctg	atg	aac	aag	gac	ctc	ggc	ctg	gcg	ctg	gcc	aac	gcc	cag	768
Val	Arg	Leu	Met	Asn	Lys	Asp	Leu	Gly	Leu	Ala	Leu	Ala	Asn	Ala	Gln	

245										250					255					
gcg	gtg	cag	gcc	tcg	acg	ccg	ctc	ggc	gcg	ctg	gcg	cgc	aac	ctg	ttc	816				
Ala	Val	Gln	Ala	Ser	Thr	Pro	Leu	Gly	Ala	Leu	Ala	Arg	Asn	Leu	Phe					
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agc	ctg	cac	gcc	cag	gcc	gat	gcc	gag	cac	gag	ggg	ctg	gac	ttc	tcc	864				
Ser	Leu	His	Ala	Gln	Ala	Asp	Ala	Glu	His	Glu	Gly	Leu	Asp	Phe	Ser					
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agc	atc	cag	aag	ctc	tac	cgc	ggc	aag	gac	taa						897				
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Gln	Pro	Lys	Ala	Val	Leu	Gly	Leu	Val	Glu	Gln	Gly	Ala	Gln	Gly	Ala					
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Asp	Ser	Ala	Leu	Gln	Cys	Cys	Glu	Gly	Ala	Glu	Val	Val	Ile	Ser	Met					
	50					55					60									
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Ile	Ala	Pro	Glu	Thr	Ala	Arg	Lys	Val	Ala	Glu	Ala	Ala	Ala	Ala	Lys					
		100						105					110							
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		115					120					125								
Arg	Ala	Gly	Thr	Leu	Ser	Phe	Ile	Val	Gly	Gly	Pro	Ala	Glu	Gly	Phe					
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Ala	Arg	Ala	Arg	Pro	Val	Leu	Glu	Asn	Met	Gly	Arg	Asn	Ile	Phe	His					
145					150					155				160						

Ala Gly Asp His Gly Ala Gly Gln Val Ala Lys Ile Cys Asn Asn Met  
165 170 175

Leu Leu Gly Ile Leu Met Ala Gly Thr Ala Glu Ala Leu Ala Leu Gly  
180 185 190

Val Lys Asn Gly Leu Asp Pro Ala Val Leu Ser Glu Val Met Lys Gln  
195 200 205

Ser Ser Gly Gly Asn Trp Ala Leu Asn Leu Tyr Asn Pro Trp Pro Gly  
210 215 220

Val Met Pro Gln Ala Pro Ala Ser Asn Gly Tyr Ala Gly Gly Phe Gln  
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Val Arg Leu Met Asn Lys Asp Leu Gly Leu Ala Leu Ala Asn Ala Gln  
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Ala Val Gln Ala Ser Thr Pro Leu Gly Ala Leu Ala Arg Asn Leu Phe  
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Ser Leu His Ala Gln Ala Asp Ala Glu His Glu Gly Leu Asp Phe Ser  
275 280 285

Ser Ile Gln Lys Leu Tyr Arg Gly Lys Asp  
290 295